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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=7; day=8; hr=8; min=28; sec=28; ms=260;]

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Application No: 09370453 Version No: 3.0

Input Set:**Output Set:**

Started: 2008-07-08 08:22:04.146
Finished: 2008-07-08 08:22:06.742
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 596 ms
Total Warnings: 65
Total Errors: 0
No. of SeqIDs Defined: 77
Actual SeqID Count: 77

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)

Input Set:

Output Set:

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Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 596 ms
Total Warnings: 65
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Actual SeqID Count: 77

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (28) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Denney, Jr., Dan W.

<120> Vaccines for Treatment of Lymphoma and Leukemia

<130> GENITOPE-03849

<140> 09370453

<141> 2008-07-08

<160> 77

<170> PatentIn version 3.3

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<210> 3

<211> 677

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<213> Simian virus 40

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 <222> (88) .. (741)

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Met Pro Thr Arg Ser Pro Ser Val Val	
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att agc gat gat gaa cca ggt tat gac cta gat ttg ttt tgt ata cct	162
Ile Ser Asp Asp Glu Pro Gly Tyr Asp Leu Asp Leu Phe Cys Ile Pro	
10 15 20 25	
aat cat tat gcc gag gat ttg gaa aaa gtg ttt att cct cat gga ctg	210
Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly Leu	
30 35 40	
att atg gac agg act gaa aga ctt gct cga gat gtc atg aag gag atg	258
Ile Met Asp Arg Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu Met	
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gga gcc cat cac att gtg gcc ctg tgt gtg ctg aag ggg gcc tat aag	306
Gly Gly His His Ile Val Ala Leu Cys Val Leu Lys Gly Gly Tyr Lys	
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Phe Phe Ala Asp Leu Leu Asp Tyr Ile Lys Ala Leu Asn Arg Asn Ser	
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Asp Arg Ser Ile Pro Met Thr Val Asp Phe Ile Arg Leu Lys Ser Tyr	
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Cys Asn Asp Gln Ser Thr Gly Asp Ile Lys Val Ile Gly Gly Asp Asp	
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ctc tca act tta act gga aag aat gtc ttg att gtt gaa gat ata att	498
Leu Ser Thr Leu Thr Gly Lys Asn Val Leu Ile Val Glu Asp Ile Ile	
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gac act ggt aaa aca atg caa act ttg ctt tcc ctg gtt aag cag tac	546
Asp Thr Gly Lys Thr Met Gln Thr Leu Leu Ser Leu Val Lys Gln Tyr	
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Ser Pro Lys Met Val Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser	
155 160 165	
cga agt gtt gga tac agg cca gac ttt gtt gga ttt gaa att cca gac	642
Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro Asp	
170 175 180 185	
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Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asn	
190 195 200	
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Leu Asn His Val Cys Val Ile Ser Glu Thr Gly Lys Ala Lys Tyr Lys	
205 210 215	

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<213> Mus musculus

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35 40 45

Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
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Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
65 70 75 80

Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
85 90 95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
100 105 110

Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
115 120 125

Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
130 135 140

Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val
145 150 155 160

Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
165 170 175

Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
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15 20 25

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Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu
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Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile
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Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser
65 70 75

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Arg Glu Leu Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser
80 85 90

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Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys
95 100 105

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Val Asp Met Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala
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160 165 170

aaa ggc atc aag tat aag ttt gaa gtc tac gag aag aaa gac 573
Lys Gly Ile Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp
175 180 185

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ccatgggact ttgctggct ttagatctat gcggccgc 671

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Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys
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Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu
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Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp
85 90 95

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